

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 9, 2003, 16:41:41 ; Search time 11 Seconds
(without alignments)
128,200 Million cell updates/sec

Sequence: 1 SVSEIQLMNLGKILNSMERVEWLKQLQDVHNF 34
US-09-843-221a-16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 6866

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	21.8	70	PF2L_PLAAPP	P07765 plasmodium
2	37	20.7	52	YOAH_HABIN	P56507 haemophilus
3	37	20.7	61	Y081_ARCFU	O30153 archaeoglob
4	36.5	20.4	54	XX13_XENLA	P40850 xenopus lae
5	36.5	20.4	59	SECE_BACLI	P38381 bacillus li
6	35	19.6	60	SENN_BACNA	P21666 bacillus su
7	35	19.6	65	SENS_BACSU	P21344 bacillus su
8	34.5	19.3	27	T4C_PASTE	Q27176 paramecium
9	34.5	19.3	61	RL37_SULSO	Q97491 sulfobolus
10	34.5	19.3	65	YNOL_RHIFR	P33214 rhizobium f
11	34.5	19.3	69	YFXX_AZOCA	P26486 azorhizobiu
12	33.5	18.7	29	GLUC_CHIBR	P31297 chinchilla
13	33.5	18.7	60	HM09_CABEL	P56407 caenorhabdi
14	33	18.4	30	PCG3_PACGO	P82416 pachycondyl
15	33	18.4	36	RL7_COXBU	O87502 coxiella bu
16	33	18.4	63	R24E_AERPE	Q99247 aeropyrum p
17	33	18.4	68	NTRC_AZOCA	Q04848 azorhizobiu
18	32.5	18.2	50	RL39_SCHPO	P05767 schizosacch
19	32	17.9	29	PCG4_PACGO	P82417 pachycondyl
20	32	17.9	59	Y423_METJA	Q57866 methanococc
21	32	17.9	62	PETL_PINTH	P52805 pinus thum
22	31	17.3	52	RL32_CVACA	O19894 cyanidium c
23	31	17.3	55	Y279_RICPR	Q92498 rickettsia
24	31	17.3	66	RL35_DEIRA	Q9rsaw6 deinococcus
25	31	17.3	68	RL29_ARCFU	O28361 archaeoglob
26	31	17.3	70	ATFJ_RAI	P29419 rattus norv
27	30.5	17.0	26	CT21_LITCI	P81847 littoria cit
28	30.5	17.0	62	RL19_NAIZE	Q08066 zea mays (m
29	30.5	17.0	64	SECE_BACHD	Q9kge8 bacillus ha
30	30	16.8	26	MEL_APIDO	P01502 apis dorsat
31	30	16.8	30	PC25_AKBL	P82144 agkistodon
32	30	16.8	42	YC70_WHEAT	Q9xpe5 triticum ae
33	30	16.8	44	SL1B_SHEEP	P07217 ovis aries

ALIGNMENTS

RESULT 1

PF2L_PLAAPP
ID PF2L_PLAAPP STANDARD; PRT; 70 AA.
AC P07765;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PF2L antigen (Fragment).
OS Plasmodium falciparum (isolate Palo Alto / Uganda).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=57270;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85242037; PubMed=2409532;
RA Langley G., Scherf A., Mercereau-Puijalon O., Koenen M., Kahane B.,
RA Mattei D., Guillothe M., Sibilli L., Garner I., Mueller-Hill B.,
RA Pereira da Silva L.;
RT "Characterisation of P. falciparum antigenic determinants isolated
RT from a genomic expression library by differential antibody
RT screening";
RL Nucleic Acids Res. 13:4191-4202(1985).
CC -! MISCELLANEOUS: THIS ANTIGEN IS EXPRESSED IN ALL ERYTHROCYTIC
CC FORMS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X02542; CAA36391.1; ALT_INIT.
CC FIR; A23809; A23809.
CC KW Malaria; Antigen.
CC FT NON TER 70
CC SEQUENCE 70 AA; 8404 MW; 21C72016A5C31023 CRC64;

Query Match 21.8%; Score 39; DB 1; Length 70;
Best Local Similarity 39.1%; Pred. No. 1.4e+02;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 5 IQLMNLGKILNSMERVEWLK 27
DB 10 IYILNNIKNLKENVDLNKR 32

RESULT 2

YOAH_HABIN
ID YOAH_HABIN STANDARD; PRT; 52 AA.
AC P56507; O86238;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein H1434.2.
GN H1434.2.

```

OS Haemophilus influenzae
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Sutton G., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT rd.";
RT Science 269:496-512(1995).
[2]
RP IDENTIFICATION.
RX MEDLINE=98248213; PubMed=9588799;
RA Rudd K.E., Humphrey-Smith I., Wasinger V.C., Bairoch A.;
RT "Low molecular weight proteins: a challenge for post-genomic
RT research.";
RL Electrophoresis 19:536-544(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0181 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; U32822; AAC23083.1; ALT_INIT.
DR TIGR; H11434.2; -.
DR InterPro; IPR005371; UPF0181.
DR Pfam; PF03701; UPF0181; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 52 AA; 5903 MW; FF8E364E185FB262 CRC64;

Query Match 20.7%; Score 37; DB 1; Length 52;
Best Local Similarity 22.2%; Pred. No. 1.9e+02;
Matches 6; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

6 QLMNIGKHLNSMERVEWLRKKIQDVH 32
: : : : : : : : : : : : : : : :
17 QIOELMAQGISGGEAIOIVAKALREIH 43

RESULT 3
Y083_ARCFU
ID Y083_ARCFU STANDARD; PRT; 61 AA.
AC O30153;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF0083.
GN AF0083.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-P., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Usterback T.,
Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RT Nature 390:364-370(1997).
RL -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; AE001100; AAB91149.1; -.
DR TIGR; AF0083; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 61 AA; 7053 MW; 4096E1B2A28E7D36 CRC64;

Query Match 20.7%; Score 37; DB 1; Length 61;
Best Local Similarity 46.2%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

2 VSEIQLMNLGKH 14
: : : : : : : : : : : : : : : :
21 ISKPLIHQTKH 33

RESULT 4
SX13_XENLA
ID SX13_XENLA STANDARD; PRT; 54 AA.
AC P40650;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE SOX-13 protein (Fragment).
GN SOX-13.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92310993; PubMed=1614875;
RA Denny P., Swift S., Brand N., Dabhadre N., Barton P., Ashworth A.;
RT "A conserved family of genes related to the testis determining gene,
RT SRV.";
RL Nucleic Acids Res. 20:2887-2887(1992).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: CONTAINS 1 HMG BOX.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; X65656; CAA46607.1; -.
DR PIR; S21491; S21491.
DR HSSP; P48436; 189M.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
DR DNA-binding; Nuclear protein.

```

```

FT NON_TER 1 1
FT DNA_BIND <1 >54 HMG BOX.
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 6612 MW; E6835BAPBC2B7731 CRC64;

Query Match 20.4%; Score 36.5; DB 1; Length 54;
Best Local Similarity 35.7%; Pred. No. 2.3e+02;
Matches 10; Conservative 5; Mismatches 4; Indels 9; Gaps 2;

QY 8 MN-----LGKH---LNSMERVWLK 26
DB 15 MNVAISKRLGKRWKMLNDSEKIPFIRE 42

RESULT 5
SECE_BACLI
ID SECE_BACLI STANDARD; PRT; 59 AA.
AC P38381;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
L- Preprotein translocase secE subunit.
GN SECE.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88139159; PubMed=3277943;
RA Dubnau E., Weir J., Nair G., Carter L. III, Moran C.P. Jr., Smith I.;
RT "Bacillus sporulation gene spoOH codes for sigma 30 (sigma H).";
RL J. Bacteriol. 170:1054-1062(1988)
CC - FUNCTION: ESSENTIAL FOR PROTEIN EXPORT.
CC - SUBCELLULAR LOCATION: Tail-anchored membrane protein (Potential).
CC - SIMILARITY: BELONGS TO THE SECE/SRC61-GAMMA FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M29694; -; NOT ANNOTATED_CDS.
DR InterPro; IPR001901; SECE.
DR InterPro; IPR004819; SecE_bac.
DR Pfam; PF00584; SECE; 1.
DR TIGRFAMs; TIGR00964; 3a0501s06; 1.
DR PROSITE; PS01067; SECE_SEC61G; 1.
KW Protein transport; Translocation; Transmembrane.
FT TRANSMEM 30 50 POTENTIAL.
SQ SEQUENCE 59 AA; 6775 MW; BD40479D9FA5837B CRC64;

Query Match 20.4%; Score 36.5; DB 1; Length 59;
Best Local Similarity 34.8%; Pred. No. 2.5e+02;
Matches 8; Conservative 6; Mismatches 6; Indels 3; Gaps 1;

QY 5 IQLMHNGLKHLNSMERVWLK 27
DB 4 IKFLKNVGK---EMKVTWPKG 23

RESULT 6
SENN_BACNA
ID SENN_BACNA STANDARD; PRT; 60 AA.
AC P21666;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Transcriptional regulatory protein senN.
GN SENN.
OS Bacillus subtilis var. natto.

```

```

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90063530; PubMed=3269394;
RA Wong S.-L., Wang L.-F., Doi R.H.;
RT "Cloning and nucleotide sequence of senN, a novel 'Bacillus natto'
RT (B. subtilis) gene that regulates expression of extracellular protein
RT genes.";
RL J. Gen. Microbiol. 134:3269-3276(1988).
CC - FUNCTION: REGULATES THE EXPRESSION OF EXTRACELLULAR-PROTEIN GENES
CC OF BACILLUS NATTO.
CC - SIMILARITY: TO SEVERAL B. SUBTILIS RNA POLYMERASE SIGMA FACTORS.
CC - SIMILARITY: TO B. SUBTILIS SENS.
DR PIR; A34945; A34945.
KW Transcription regulation; DNA-binding.
FT DNA_BIND 11 31 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 60 AA; 7220 MW; OCE30106C062B6F6 CRC64;

Query Match 19.6%; Score 35; DB 1; Length 60;
Best Local Similarity 27.8%; Pred. No. 4e+02;
Matches 8; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 4 EIQLMHNGLKHLNSMERVWLK 32
DB 26 ELLIEKVKREIINSALMEIYMKIDKH 54

RESULT 7
SENS_BACSU
ID SENS_BACSU STANDARD; PRT; 65 AA.
AC P21344;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transcriptional regulatory protein sens.
GN SENS.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90202712; PubMed=2108127;
RA Wang L.-F., Doi R.H.;
RT "Complex character of sens, a novel gene regulating expression of
RT extracellular-protein genes of Bacillus subtilis.";
RL J. Bacteriol. 172:1939-1947(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97346037; PubMed=9202460;
RA Cummings N.J., Connerton I.F.;
RT "The Bacillus subtilis 168 chromosome from sspE to katA.";
RL Microbiology 143:1855-1859(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duisterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Colightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

```

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudesa B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Fujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone P.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seiror P., Shin B.S., Soldo B.,
 RA Sorokin A., Taconni E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Tosiato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.P., Zumstein E., Yoshikawa H., Danchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256 (1997).
 CC -!- FUNCTION: REGULATES THE EXPRESSION OF EXTRACELLULAR-PROTEIN GENES
 CC OF BACILLUS SUBTILIS.
 CC -!- SIMILARITY: TO SEVERAL B. SUBTILIS RNA POLYMERASE SIGMA FACTORS.
 CC -!- SIMILARITY: TO B.NATTO SENN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M34826; AAA22750.1; -;
 DR EMBL; Z82044; CAB04806.1; -;
 DR EMBL; Z99108; CAB12709.1; ALT_INIT.
 DR PIR; A35150; A35150.
 DR Subtilisin; BG10747; sens.
 KW Transcription regulation; DNA-binding; Complete proteome.
 FT DNA BIND 11 31 H-T-H MOTIF (BY SIMILARITY).
 SQ SEQUENCE 65 AA; 7912 MW; 4A685B04179CE318 CRC64;
 Query Match 19.6%; Score 35; DB 1; Length 65;
 Best Local Similarity 27.6%; Pred. No. 4.4e+02;
 Matches 8; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 4 EIQLMHNLGKHLNSMERVWLKQLQDVH 32
 DB 26 ELLIEKRNREIINSALMEIYMKIDEXH 54
 P<0.001
 PART 8
 T4C PARTE STANDARD; PRT; 27 AA.
 AC Q27176;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Trichocyst matrix protein T4-C (Secretory granule protein T4-C)
 DE (T4P 4-C) (Fragment).
 GN T4C.
 OS Paramecium tetraurelia.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 OC Paramecium.
 OX NCBI_TaxID=5889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D4-2;
 RX MEDLINE=96059477; PubMed=7579685;
 RA Madeddu L., Gautier M.-C., Vayssie L., Houari A., Sperling L.;
 RT "A large multigene family codes for the polypeptides of the
 RL crystalline trichocyst matrix in Paramecium.";
 RL Mol. Biol. Cell 6:649-659 (1995).
 RN [2]
 RP PARTIAL SEQUENCE.
 RC STRAIN=D4-2;
 RX MEDLINE=95119139; PubMed=7819344;

RA Madeddu L., Gautier M.-C., le Caer J.P., de Loubresse N., Sperling L.;
 RT "Protein processing and morphogenesis of secretory granules in
 RL Paramecium.";
 RL Biochimie 76:329-335 (1994).
 CC -!- FUNCTION: STRUCTURAL PROTEIN THAT CRYSTALLIZE INSIDE THE
 CC TRICHO CYST MATRIX.
 CC -!- SUBCELLULAR LOCATION: TRICHO CYST. THESE ARE ARCHITECTURALLY
 CC COMPLEX SECRETORY STORAGE GRANULES-DOCKED AT THE PLASMA MEMBRANE,
 CC READY TO RAPIDLY RESPOND TO AN EXOCYTOTIC STIMULUS.
 CC -!- SIMILARITY: BELONGS TO THE TMP FAMILY.
 CC -!- DATABASE: NAME-Protein Spotlight;
 CC NOTE=Issue 3 of October 2000;
 CC WWW="http://www.expasy.org/spotlight/articles/sptlt003.html".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U27514; AAA92614.1; -;
 KW Polyprotein; Structural protein; Multigene family.
 FT NON_TER 1 1
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2837 MW; 731046E30185A542 CRC64;
 Query Match 19.3%; Score 34.5; DB 1; Length 27;
 Best Local Similarity 38.1%; Pred. No. 2.1e+02;
 Matches 8; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
 QY 1 SVSEIQ-LMHNGLKHLNSMER 20
 DB 2 AVGEIQILLNNIASQLNGDQX 22
 RESULT 9
 ID<0.001
 RL37_SULSO STANDARD; PRT; 61 AA.
 AC Q972Q1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L37e.
 GN RPL37E OR SSO6453.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Aweze M.J., Chan-Weiner C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Brauso G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozeza C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
 RA "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).
 CC -!- SIMILARITY: BELONGS TO THE L37E FAMILY OF RIBOSOMAL PROTEINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC

```

DR EMBL; AB006699; AAK41052.1; --
DR InterPro; IPR001569; Ribosomal L37E.
DR Pfam; PF01907; Ribosomal L37e; 1.
DR ProDom; PD005132; Ribosomal L37E; 1.
DR PROSITE; PS01077; RIBOSOMAL_L37E; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 61 AA; 7145 MW; FF9BFCDE4FD4805A CRC64;

Query Match
Best Local Similarity 19.3%; Score 34.5; DB 1; Length 61;
Matches 8; Conservative 4; Mismatches 11; Indels 9; Gaps 1;

QY 9 HNLGKH-----LNSMERVEWLKRLQDV 31
Db 27 YNVSKHYCAACGPGRTKIRRYSWQNKVNGV 58

RESULT 10
YNOL RHIFR STANDARD; PRT; 65 AA.
ID YNOL RHIFR
I 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DS Hypothetical 7.1 kDa protein in nolu-nolv intergenic region (ORF4).
OS Rhizobium fredii (Sinorhizobium fredii).
OC Plasmid sym.
CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=380;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-USDA 257;
RX MEDLINE=94018604; PubMed=8412662;
RA Meinhardt L.W., Krishnan H.B., Balatti P.A., Pueppke S.G.;
RT "Molecular cloning and characterization of a sym plasmid locus that
RT regulates cultivar-specific nodulation of soybean by Rhizobium fredii
RT USDA257.";
RL Mol. Microbiol. 9:17-29(1993).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X55450; CAA39095.1; --
DR PIR; S14074; S14074.
KW Hypothetical protein; Nitrogen fixation.
SQ SEQUENCE 69 AA; 7721 MW; 15CBC9E2B229B5A6 CRC64;

Query Match
Best Local Similarity 19.3%; Score 34.5; DB 1; Length 69;
Matches 11; Conservative 10; Mismatches 10; Indels 15; Gaps 1;

QY 1 SVSEIQLMHNIGKHL-----NSMERVEWLKRLQDV 31
Db 18 SVNAKNLHLSDDLPTNWQSIIEVAQETNTFTKLEDAKKLQKEL 63

RESULT 12
GLUC_CHIBR STANDARD; PRT; 29 AA.
ID GLUC_CHIBR
AC F31297;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucagon.
CG
GN Chinchilla brevicaudata (Chinchilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
OC Chinchilla.
OX NCBI_TaxID=10152;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045327; PubMed=2235678;
RA Eng J., Kleinman W.A., Chu L.S.;
RT "Purification of peptide hormones from chinchilla pancreas by
RT chemical assay.";
RL Peptides 11:683-685(1990).
CC
CC -1- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.
CC -1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
CC
CC PIR; A60413; GCCB.
DR HSSP; P01275; 1BH0.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF0123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone.
SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match
Best Local Similarity 18.7%; Score 33.5; DB 1; Length 29;
Matches 5; Conservative 6; Mismatches 12; Indels 5; Gaps 1;

QY 3 SEIQLMHNIGKHLNSERVE-----WLKRLQ 29
Db 24 SELNIWHSAGDALAAAKRHQQRVTRWAAYQ 55

RESULT 11
YFXX AZOCA STANDARD; PRT; 69 AA.
ID YFXX AZOCA
AC P26486;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DS Hypothetical 7.7 kDa protein in FIXX 3'region (ORF1).
OS Azorhizobium caulinodans.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae group; Azorhizobium.
OX NCBI_TaxID=7;

```

```
Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;
QY 13 KHLNS---MERVEWL 24
DB 12 KHLDSRYAQEPVQWL 26
RESULT 13
HM09 CAEL STANDARD; PRT; 60 AA.
AC PS6407;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Homeobox protein ceh-9 (Fragment).
GN CEB-9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=91045075; PubMed=1978282;
RA Hawkins N.C., McGhee J.D.;
RT "Homeobox containing genes in the nematode Caenorhabditis elegans.";
RL Nucleic Acids Res. 18:6101-6106(1990).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DB EMBL; X52811; CAB57217.1; -
DR HSSP; P14653; 1B72.
DR TRANSFAC; T02979; -.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD00010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 60
FT DNA_BIND 1 60
FT NON_TER 60 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 7308 MW; 04175DFAAF5430B4 CRC64;
Query Match 18.7%; Score 33.5; DB 1; Length 60;
Best Local Similarity 37.0%; Pred. No. 6.2e+02;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
QY 2 VSEIQLMNLGKHLNSMERVEWLKKL 28
DB 13 VFELEKQFEAKKYLSSDRSE-LAKRL 38
RESULT 14
PCG3 PACGO STANDARD; PRT; 30 AA.
AC B92416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ponericin G3.
OS Pachycondyla goeldii (Ponerine ant.).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Formicidae; Ponerinae; Pachycondyla.
NCBI_TaxID=118888;
[1]
SEQUENCE, AND FUNCTION.
RP TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -1- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -1- MASS SPECTROMETRY: MW=3381.36; METHOD=WALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;
Query Match 18.4%; Score 33; DB 1; Length 30;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 8; Gaps 1;
QY 10 NLGKHLNSMERVEWLKK 27
DB 7 NKGK-----EMLKK 16
RESULT 15
RL7 COXBU STANDARD; PRT; 36 AA.
AC OB7902;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L7/L12 (Fragment).
GN RPL1.
OS Coccidia burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coccidia group; Coccidia.
OX NCBI_TaxID=777;
[1]
SEQUENCE FROM N.A.
RX STRAIN=Q212;
RX MEDLINE=98172740; PubMed=9511749;
RA Mollet C., Drancourt M., Raoult D.;
RT "Determination of Coccidia burnetii rpoB sequence and its use for
RT phylogenetic analysis.";
RL Gene 207:97-103(1998).
[2]
CONCEPTUAL TRANSLATION.
RA Veuthey A.-L.;
RL Unpublished observations (MAR-2000).
CC -1- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS
CC INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR
CC ACCURATE TRANSLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
CC INTRODUCED IN POSITION 10 TO PRODUCE THIS ORF.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DB EMBL; U86688; AAC61665.1; ALT_FRAME.
DR InterPro; IPR00206; Ribosomal L12.
DR Pfam; PF00542; Ribosomal_L12; 1.
KW Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 36 AA; 3930 MW; 4C1AB1ED69FB8073 CRC64;
Query Match 18.4%; Score 33; DB 1; Length 36;
```

Best Local Similarity 30.8%; Pred. No. 4.3e+02;
Matches 8; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 5 IQLMHNIGKHLNSMERVEWLRKKLQD 30
Db 3 VESVPSVVKESVSKERAEKLRKSLLE 28

Search completed: April 9, 2003, 16:44:37
Job time : 18 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 9, 2003, 16:42:41 ; Search time 28 Seconds
(without alignments)
250,200 Million cell updates/sec

File: US-09-843-221A-16
Perfect score: 179
Sequence: 1 SVSEIQLMNLGKLNLSERVEWLKQLQDVHNF 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 60947

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database: SPRENBL21
- 1: sp_bacteria.*
 - 2: sp_fungi.*
 - 3: sp_human.*
 - 4: sp_invertebrate.*
 - 5: sp_mammal.*
 - 6: sp_mhc.*
 - 7: sp_organelle.*
 - 8: sp_phase.*
 - 9: sp_plant.*
 - 10: sp_rodent.*
 - 11: sp_virus.*
 - 12: sp_vertebrate.*
 - 13: sp_unclassified.*
 - 14: sp_rvirus.*
 - 15: sp_bacteriaph.*
 - 16: sp_archae.*
 - 17: sp_archae.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	85	47.5	31 11 Q91Y91	Q91Y91 peromyscus	
2	85	47.5	31 11 Q91Y90	Q91Y90 peromyscus	
3	49.5	27.7	60 6 Q9BDL8	Q9BDL8 phocoenoid	
4	47	26.3	63 10 Q9LH68	Q9LH68 arabidopsis	
5	43.5	24.3	68 6 Q9BG71	Q9BG71 canis fami	
6	41.5	23.2	58 5 Q94768	Q94768 strongyloce	
7	41	22.9	53 7 Q30452	Q30452 equus asinu	
8	40	22.3	40 5 Q27099	Q27099 trichomonas	
9	40	22.3	52 8 Q35600	Q35600 paratetetic	
10	40	22.3	70 4 Q9BU57	Q9BU57 homo sapien	
11	39.5	22.1	54 16 Q9ZIK1	Q9ZIK1 rickettsia	
12	39	21.8	40 5 Q27098	Q27098 trichomonas	
13	39	21.8	52 8 Q34854	Q34854 lampronia a	
14	39	21.8	70 7 Q8SNL4	Q8SNL4 rivulus mar	
15	39	21.8	70 7 Q8SNL3	Q8SNL3 rivulus mar	
16	39	21.8	70 7 Q8SNL0	Q8SNL0 rivulus mar	

17	39	21.8	70 7 Q8SNK9	Q8snk9 rivulus mar
18	39	21.8	70 7 Q8SNK8	Q8snk8 rivulus mar
19	39	21.8	70 7 Q8SNK7	Q8snk7 rivulus mar
20	39	21.8	70 7 Q8SNK6	Q8snk6 rivulus mar
21	39	21.8	70 7 Q8SNK5	Q8snk5 rivulus mar
22	39	21.8	70 7 Q8SNK4	Q8snk4 rivulus mar
23	39	21.8	70 7 Q8SNK3	Q8snk3 rivulus mar
24	39	21.8	70 7 Q8SNK2	Q8snk2 rivulus mar
25	39	21.8	70 7 Q8SNK1	Q8snk1 rivulus mar
26	39	21.8	70 7 Q8SNK0	Q8snk0 rivulus mar
27	39	21.8	70 7 Q8SNJ9	Q8snj9 rivulus mar
28	39	21.8	70 7 Q8SNJ8	Q8snj8 rivulus mar
29	39	21.8	70 7 Q8SNJ7	Q8snj7 rivulus mar
30	39	21.8	70 7 Q8SNJ6	Q8snj6 rivulus mar
31	39	21.8	70 7 Q8SNJ5	Q8snj5 rivulus mar
32	39	21.8	70 7 Q8SNJ4	Q8snj4 rivulus mar
33	38.5	21.5	56 17 Q8TZD8	Q8tzd8 pyrococcus
34	38.5	21.5	61 16 Q9JUI4	Q9juui4 neisseria m
35	38	21.2	40 5 Q27233	Q27233 trichomonas
36	38	21.2	50 2 Q8ROK9	Q8rqk9 bacillus ce
37	38	21.2	52 8 Q34628	Q34628 greya powel
38	38	21.2	52 8 Q34680	Q34680 greya varia
39	38	21.2	56 16 Q8RAP7	Q8rap7 thermoanaer
40	38	21.2	61 2 Q9X9G5	Q9x9g5 yersinia ps
41	38	21.2	68 16 Q8X414	Q8x414 escherichia
42	37.5	20.9	45 5 Q94693	Q94693 polycelis n
43	37.5	20.9	58 16 Q8XLW5	Q8xlw5 clostridium
44	37.5	20.9	69 17 Q26627	Q26627 methanobact
45	37	20.7	48 7 Q98171	Q98171 melopsittac

ALIGNMENTS

RESULT 1

Q91Y91 ID Q91Y91 PRELIMINARY; PRT; 31 AA.

AC Q91Y91; DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Parathyroid hormone (Fragment).

GN PTH.

OS Peromyscus polionotus (Oldfield mouse).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Peromyscus.

OX NCBI_TaxID=42413;

RN [1] SEQUENCE FROM N.A.

RP Prince K.L., Dewey M.J.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF382952; AAK63071.1;

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; Pthyrdorm_sub.

DR	Pfam; PFO1279; Parathyroid; 1.
DR	ProDom; PD010687; Pthyrdorm sub; 1.
DR	PROSITE; PS00335; PARATHYROID; UNKNOWN_1.
FT	NON_TER 1 1
FT	NON_TER 31 31
SQ	SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 47.5%; Score 85; DB 11; Length 31;

Best Local Similarity 89.5%; Pred. No. 0.00027;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMNLGKLNLSERVEWLKQLQDVHNF 19

Db 13 AVSEIQLMNLGKLNLSERVEWLKQLQDVHNF 31

RESULT 2

Q91Y90

```

RESULT 4
Q9LH68 PRELIMINARY; PRT; 63 AA.
ID Q9LH68;
AC Q9LH68;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Gb|AAD27902.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
NCBI_TaxId=3702;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=COLUMBIA;
RC Nakamura Y.;
RA "Structural Analysis of Arabidopsis thaliana Chromosome 3. III.";
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF002062; BAB02653.1; -
RD SEQUENCE 63 AA; 7025 MW; 2C8966DBEB4673DD CRC64;
SQ
Query Match 26.3%; Score 47; DB 10; Length 63;
Best Local Similarity 47.1%; Pred. No. 57;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 7 LMHNLGKHLNSMRVSV 23
DB 38 LNNLNGKHPNKVIQTW 54
:::|||||:::|

RESULT 5
Q9BG71 PRELIMINARY; PRT; 68 AA.
ID Q9BG71
AC Q9BG71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 10 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxId=9615;
RX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=BLOOD;
RC Markus S., Groene A., Baumgaertner W.;
RA "Expression of canine interleukin-10 mRNA in concanavalin A-stimulated
RT canine lymphocytes.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RD EMBL; AF333120; AAK01440.1; -
DE HSPSP; P22301.1INR.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
FT NON_TER 1 1
FT NON_TER 68 68
SQ SEQUENCE 68 AA; 7920 MW; AF916BEB1EAA438C CRC64;

Query Match 24.3%; Score 43.5; DB 6; Length 68;
Best Local Similarity 34.6%; Pred. No. 1.8e+02;
Matches 9; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 10 NLGKHLNSM-ERVEWLRRKKLQDVNF 34
DB 27 DIKNVNSLGKTKTLRLRLRRCHRF 52
:::|||||:::|

RESULT 6
Q94768 PRELIMINARY; PRT; 58 AA.
ID Q94768

```

Q94768;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Rabi1 GTPase homolog SURAB1p (Fragment).
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Leaf D.S.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88769; BAB09700.1; -;
 DR HSSP; P17080; IAK2.
 DR InterPro; IPR001806; Ras trnsfrmg.
 DR InterPro; IPR003575; Small_GTPase.
 DR Pfam; PF00071; ras; 1.
 DR SMART; SM00010; small_GTPase; 1.
 FT NON_TER 1 1
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6770 MW; 09086186050D76E3 CRC64;
 Query Match 23.2%; Score 41.5; DB 5; Length 58;
 Best Local Similarity 48.0%; Pred. No. 2.8e+02;
 Matches 12; Conservative 7; Mismatches 3; Indels 3; Gaps 3;
 QY 7 LMNIGKHLNSMERVE-WLRKKLQD 30
 DB 20 LVYDIAGHL-TYENVERWL-KELRD 42
 RESULT 7
 Q30452
 ID Q30452 PRELIMINARY; PRT; 53 AA.
 AC Q30452;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II HLA-DOB1 antigen (Fragment).
 OS Equus asinus (Donkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9793;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nasir L., Stear M.J., Reid S.W.J.;
 "Nucleotide sequence of the Donkey MHC DOB first domain exon."
 Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U31774; AAA86414.1; -;
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 53 53
 SQ SEQUENCE 53 AA; 6406 MW; 9DA1C857BC30DDA1 CRC64;
 Query Match 22.9%; Score 41; DB 7; Length 53;
 Best Local Similarity 34.6%; Pred. No. 3e+02;
 Matches 9; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
 QY 2 VSEIQLMHNIGKHLNSMERVEWLRKK 27
 DB 24 VGEFQAVTELGRHIAE----DWNQK 45
 RESULT 8
 Q27099
 ID Q27099 PRELIMINARY; PRT; 40 AA.
 AC Q27099;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ubiquitin (Fragment).
 GN UBI1.
 OS Trichomonas vaginalis.
 OC Eukaryota; Parabasalidea; Trichomonadida; Trichomonadidae;
 OC Trichomonas.
 OX NCBI_TaxID=5722;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH-C1;
 RA Keeling P.J., Doolittle W.P.;
 RL MEDLINE=96081479; PubMed=7490769;
 RT "Concerted evolution in protists: recent homogenization of a
 polyubiquitin gene in Trichomonas vaginalis.";
 RL J. Mol. Evol. 41:556-562(1995).
 DR EMBL; U28011; AAC46939.1; -;
 DR HSSP; P02248; 1UBI.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; ubiquitin; 1.
 DR PROSITE; PS50053; UBIQUITIN_2; 1.
 FT NON_TER 1 1
 FT NON_TER 40 40
 SQ SEQUENCE 40 AA; 4530 MW; 5ADDA65EEEC2DALA CRC64;
 Query Match 22.3%; Score 40; DB 5; Length 40;
 Best Local Similarity 34.8%; Pred. No. 3e+02;
 Matches 8; Conservative 7; Mismatches 4; Indels 4; Gaps 1;
 QY 12 GKHL-----NSMERVEWLRKKLQD 30
 DB 4 GKHTLDVESADKIEDVKAKIQD 26
 RESULT 9
 Q35600
 ID Q35600 PRELIMINARY; PRT; 52 AA.
 AC Q35600;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment).
 OS Parategeticula pollenifera.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Incurvarioidea; Prodoxidae; Parategeticula.
 OX NCBI_TaxID=30238;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SANTA CRUZ CO;
 RA Brown J.M., Pellmyr O., Thompson J.N., Harrison R.G.;
 RT "Mitochondrial DNA phylogeny of the Prodoxidae (Lepidoptera:
 Incurvarioidea) indicates rapid ecological diversification of yucca
 moths.";
 RL Ann. Entomol. Soc. Amer. 87:795-802(1994).
 DR EMBL; U04884; AAA16151.1; -;
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 52 AA; 6105 MW; C4E2ED2351EC5ED1 CRC64;
 Query Match 22.3%; Score 40; DB 8; Length 52;
 Best Local Similarity 35.0%; Pred. No. 3.9e+02;
 Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 15 LNSMERVEWLRKKLQDVNF 34
 DB 24 LNTSSIEWLQKFPPTSHY 43
 RESULT 10
 Q9BU57
 ID Q9BU57 PRELIMINARY; PRT; 70 AA.

```

AC Q9BU57;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Similar to cofactor required for Spl transcriptional activation,
DE subunit 8 (34kD).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Srausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002878; AA02878.1; -.
SQ SEQUENCE 70 AA; 8019 MW; 83AC87EA4760E384 CRC64;

Query Match 22.3%; Score 40; DB 4; Length 70;
Best Local Similarity 32.0%; Pred. No. 5.3e+02;
Matches 8; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 8 MHNLGKHLNSMERVEWLKKLQDVH 32
   : : : : : : : : : : : : : :
Db 22 LHSVNRDLNELRLSLNVLGKPSNH 46

RESULT 11
Q92IK1 PRELIMINARY; PRT; 54 AA.
ID Q92IK1;
AC Q92IK1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein RC0419.
GN RC0419.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RA "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
DR EMBL; AB008606; AA02957.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 54 AA; 6120 MW; 063655E7022C28C0 CRC64;

Query Match 22.1%; Score 39.5; DB 16; Length 54;
Best Local Similarity 37.0%; Pred. No. 4.8e+02;
Matches 10; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

Qy 5 IQLMNLGKHLNSMERVEWLKKLQDV 31
   : : : : : : : : : : : : : :
Db 15 IEVMHYIFGLHS-EKSTVSSKKVTEI 40

RESULT 12
Q27098 PRELIMINARY; PRT; 40 AA.
ID Q27098;
AC Q27098;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Ubiquitin (Fragment).
GN UBI1A
OS Trichomonas vaginalis.
OC Eukaryota; Parabasalidae; Trichomonadida; Trichomonadidae;

```

```

OC Trichomonas.
OX NCBI_TaxID=5722;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH-C1;
RX MEDLINE=96081479; PubMed=7490769;
RA Keeling P.J., Doolittle W.F.;
RA "Concerted evolution in protists: recent homogenization of a
RA polyubiquitin gene in Trichomonas vaginalis.";
J. Mol. Evol. 41:556-562(1995).
RL EMBL; U28008; AAC46936.1; -.
DR HSSP; P02248; 1UBI.
DR InterPro; IPR00626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR PROSITE; PS00553; UBIQUITIN_2; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4528 MW; 46843B0C9BF0E7EA CRC64;

Query Match 21.8%; Score 39; DB 5; Length 40;
Best Local Similarity 34.8%; Pred. No. 4.1e+02;
Matches 8; Conservative 6; Mismatches 5; Indels 4; Gaps 1;

Qy 12 GKHL----NSMERVEWLKKLQD 30
   : : : : : : : : : : : : : :
Db 4 GKHTLEVEPTDRIEVVKAKIQD 26

RESULT 13
Q34854 PRELIMINARY; PRT; 52 AA.
ID Q34854;
AC Q34854;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Lampronia aenesens.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Incurvarioidea; Prodoxidae; Lampronia.
OX NCBI_TaxID=30234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GARFIELD CO;
RA Brown J.M., Fellmyr O., Thompson J.N., Harrison R.G.;
RA "Mitochondrial DNA phylogeny of the Prodoxidae (Lepidoptera:
RA Incurvarioidea) indicates rapid ecological diversification of yucca
RA moths.";
Ann. Entomol. Soc. Amer. 87:795-802(1994).
RL EMBL; U04889; AAA16085.1; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 52 AA; 6043 MW; 45BA2FC4FE22B094 CRC64;

Query Match 21.8%; Score 39; DB 8; Length 52;
Best Local Similarity 30.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 15 LNSMERVEWLKKLQDVHNF 34
   : : : : : : : : : : : : : :
Db 24 LNTISIEWLQNSPPAEHSY 43

RESULT 14
Q8SNL4 PRELIMINARY; PRT; 70 AA.
ID Q8SNL4;
AC Q8SNL4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MHC class I antigen (Fragment).
OS Rivulus marmoratus (mangrove rivulus).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Rivulus.
OX NCBI_TaxID=37003;
RN [1]
RP SEQUENCE FROM N.A.
RA Fisher M.T., Turner B.J.;
RT "Variation at MHC class I loci in a naturally homozygous vertebrate,
the killifish Rivulus marmoratus.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF365267; AAL99671.1; -
FT NON TER 1
FT NON TER 70
SQ SEQUENCE 70 AA; 8315 MW; 07FB2822AC186C0B CRC64;

Query Match 21.8%; Score 39; DB 7; Length 70;
Best Local Similarity 24.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

2 VSEIQLMHNIGKHLNSMERVWLK 26
10 VDEVQMFHYDSNTWKAEPKQDWMK 34

RESULT 15
Q8SNL3 PRELIMINARY; PRT; 70 AA.
AC Q8SNL3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MHC class I antigen (Fragment).
OS Rivulus marmoratus (mangrove rivulus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Rivulus.
OX NCBI_TaxID=37003;
RN [1]
RP SEQUENCE FROM N.A.
RA Fisher M.T., Turner B.J.;
RT "Variation at MHC class I loci in a naturally homozygous vertebrate,
the killifish Rivulus marmoratus.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF365268; AAL99672.1; -
FT NON TER 1
FT NON TER 70
SQ SEQUENCE 70 AA; 8281 MW; 0F518A22AC1682EB CRC64;

Query Match 21.8%; Score 39; DB 7; Length 70;
Best Local Similarity 24.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

2 VSEIQLMHNIGKHLNSMERVWLK 26
10 VDEVQMFHYDSNTWKAEPKQDWMK 34

Search completed: April 9, 2003, 16:45:06
Job time : 29 secs

THIS PAGE BLANK (USPTO)

Result No.	Score	Query Match	Length	DB	ID	Description
1	179	100.0	34	9	US-09-928-047B-6	Sequence 6, Appl
2	179	100.0	34	9	US-09-843-221A-16	Sequence 16, Appl
3	179	100.0	34	9	US-09-843-221A-61	Sequence 61, Appl
4	179	100.0	34	10	US-09-163-786-3	Sequence 3, Appl
5	179	100.0	34	12	US-10-016-403-5	Sequence 5, Appl
6	179	100.0	34	12	US-10-097-079-1	Sequence 1, Appl
7	179	100.0	38	9	US-09-843-221A-14	Sequence 14, Appl
8	179	100.0	38	10	US-09-163-786-4	Sequence 4, Appl
9	179	100.0	42	9	US-10-024-918-28	Sequence 28, Appl
10	179	100.0	44	9	US-09-843-221A-13	Sequence 13, Appl
11	175	97.8	34	9	US-09-843-221A-20	Sequence 20, Appl
12	175	97.8	37	9	US-09-843-221A-15	Sequence 15, Appl
13	174	97.2	34	9	US-09-843-221A-19	Sequence 19, Appl
14	174	97.2	34	9	US-09-843-221A-164	Sequence 164, Appl
15	174	97.2	34	12	US-10-016-403-6	Sequence 6, Appl
16	174	97.2	34	12	US-10-016-403-7	Sequence 7, Appl
17	173	96.6	34	9	US-09-843-221A-17	Sequence 17, Appl
18	173	96.6	34	9	US-09-843-221A-18	Sequence 18, Appl
19	173	96.6	34	9	US-09-843-221A-162	Sequence 162, Appl

ALIGNMENTS

```

RESULT 1
US-09-928-047B-6
; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-6

```

Query Match	100.0%	Score 179;	DB 9;	Length 34;
Best Local Similarity	100.0%	Pred. NO. 1.9e-17;		
Matches 34;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SVSEIQLMNLGKHLNSMERVEWLKKLQDVHNF	34	
Dh	1	SVSEIQLMNLGKHLNSMERVEWLKKLQDVHNF	34	

RESULT 2
US - 09-843-221A-16
Sequence 16, Application US/09843221A
Publication No. US20030039654A1
GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CHUAN-PA
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RE
TITLE OF INVENTION: RELATED PROTEIN
FILE REFERENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843

; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-843-221A-16

Query Match 100.0%; Score 179; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3
 US-09-843-221A-161
 ; Sequence 161, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENIUK, PAUL
 ; APPLICANT: LIU, CHUAN-PA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 161
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Preferred embodiments - PTH
 ; NAME/KEY: misc feature
 ; LOCATION: (34)-(34)
 ; OTHER INFORMATION: Optional linker and PC domain attached at the C-terminus
 US-09-843-221A-161

Query Match 100.0%; Score 179; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 4
 US-09-169-786-3
 ; Sequence 3, Application US/09169786B
 ; Patent No. US2002025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480

; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-169-786-3

Query Match 100.0%; Score 179; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 5
 US-10-016-403-5
 ; Sequence 5, Application US/10016403
 ; Patent No. US20020107505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holladay, Leslie A.
 ; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
 ; INCREASE ELECTROTRANSPORT FLUX
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
 ; STREET: 25 West Main Street
 ; CITY: Madison
 ; STATE: WI
 ; COUNTRY: USA
 ; ZIP: 53701-2236

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/016,403
 ; FILING DATE: 10-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/466,610
 ; FILING DATE: 1995-JUN-06
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Frenchick, Grady J.
 ; REGISTRATION NUMBER: 29,018
 ; REFERENCE/DOCKET NUMBER: 8734.28
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 608-257-2281
 ; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1..34
 ; OTHER INFORMATION: /note= "parathyroid hormone"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-10-016-403-5

Query Match 100.0%; Score 179; DB 12; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

Db 1 SVSEIQLMHNHKGHLNSMERVEWLKQLQDVHNF 34
 |||||
 RESULT 6
 US-10-097-079-1
 ; Sequence 1, Application US/10097079
 ; Patent No. US20020132973A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Condon, Stephen M.
 ; ; Morize, Isabelle
 ; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, Mailstop 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/097,079
 ; FILING DATE: 13-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/228,990
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 60/046,472
 ; FILING DATE: 14-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Martin Esq., Michael B.
 ; REGISTRATION NUMBER: 37,521
 ; REFERENCE/DOCKET NUMBER: A2678B-WO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-2793
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: No. US20020132973A1 Relevant
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: N-terminal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-097-079-1
 Query Match 100.0%; Score 179; DB 12; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SVSEIQLMHNHKGHLNSMERVEWLKQLQDVHNF 34
 |||||
 Db 1 SVSEIQLMHNHKGHLNSMERVEWLKQLQDVHNF 34
 |||||
 RESULT 7
 US-09-843-221a-14
 ; Sequence 14, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENIUK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-843-221A-14
 Query Match 100.0%; Score 179; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SVSEIQLMHNHKGHLNSMERVEWLKQLQDVHNF 34
 |||||
 Db 1 SVSEIQLMHNHKGHLNSMERVEWLKQLQDVHNF 34
 |||||
 RESULT 8
 US-09-169-786-4
 ; Sequence 4, Application US/09169786B
 ; Patent No. US2002025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-169-786-4
 Query Match 100.0%; Score 179; DB 10; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SVSEIQLMHNHKGHLNSMERVEWLKQLQDVHNF 34
 |||||
 Db 1 SVSEIQLMHNHKGHLNSMERVEWLKQLQDVHNF 34
 |||||
 RESULT 9
 US-10-024-918-28
 ; Sequence 28, Application US/10024918
 ; Patent No. US20020168718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hubbell, Jeffrey
 ; APPLICANT: Schense, Jason
 ; APPLICANT: Zisch, Andreas
 ; APPLICANT: Hall, Heike
 ; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
 ; FILE REFERENCE: CIT 2606 CIP
 ; CURRENT APPLICATION NUMBER: US/10/024,918
 ; CURRENT FILING DATE: 2001-12-18
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 28
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:

RESULT 11
US-09-843-221A-20
; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843, 221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266, 673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214, 860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200, 053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 34

```

; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-19

Query Match          97.2%; Score 174; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 8.7e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNIGKHLNSMERVWLKKLQDVHNF 34
Db 1 SVSEIQLMHNIGKHLNSMERVWLKKLQDVHNF 34

RESULT 14
US-09-843-221A-164
; Sequence 164, Application US/09843221A
; Publication No. US20030039654A1
; SERIAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-PA
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 164
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-164

Query Match          97.2%; Score 174; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 8.7e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNIGKHLNSMERVWLKKLQDVHNF 34
Db 1 SVSEIQLMHNIGKHLNSMERVWLKKLQDVHNF 34

RESULT 15
US-10-016-403-6
; Sequence 6, Application US/10016403
; Patent No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-403-6

Query Match          97.2%; Score 174; DB 12; Length 34;
Best Local Similarity 97.1%; Pred. No. 8.7e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNIGKHLNSMERVWLKKLQDVHNF 34
Db 1 SVSEIQLMHNIGKHLNSMERVWLKKLQDVHNF 34

Search completed: April 9, 2003, 16:46:12
Job time : 15 secs

```

THIS PAGE BLANK (USPTO)

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	40	22.3	57	2	C53260	hypothetical prote
2	39.5	22.1	54	2	C97752	hypothetical prote
3	39	21.8	70	2	A23809	160K antigen - mal
4	38.5	21.5	61	2	A81898	hypothetical prote
5	38	21.2	55	2	S43483	hypothetical prote
6	38	21.2	60	2	D44088	homeotic protein H
7	38	21.2	61	2	T47055	hypothetical prote
8	38	21.2	68	2	F85909	hypothetical prote
9	37.5	20.9	69	2	E69169	hypothetical prote
10	37	20.7	61	2	C62660	hypothetical prote
11	37	20.7	62	2	AI2130	hypothetical prote
12	37	20.7	64	2	B69175	hypothetical prote
13	36	20.1	55	2	A84180	hypothetical prote
14	36	20.1	68	2	G82027	hypothetical prote
15	36	20.1	70	2	E90872	hypothetical prote
16	36	20.1	70	2	F85746	unknown protein en
17	35.5	19.8	34	2	G84147	hypothetical prote
18	35.5	19.8	40	2	S71295	deoxyguanosine kin
19	35.5	19.8	52	2	T00141	hypothetical prote
20	35.5	19.8	54	2	S22948	SOX-13 protein - A
21	35	19.6	51	2	C69153	hypothetical prote
22	35	19.6	52	2	S52069	p36 protein (CAK c
23	35	19.6	58	2	AH1092	hypothetical prote
24	35	19.6	60	2	A34945	transcription regu
25	35	19.6	61	2	AH3198	hypothetical prote
26	34.5	19.3	51	2	A56785	calmodulin - pig (
27	34.5	19.3	59	2	H82107	hypothetical prote
28	34.5	19.3	61	2	E90224	18S ribosomal prot
29	34.5	19.3	65	2	S35024	hypothetical prote

QY 5 IQLMHNGLKHLNSMERVEWLRLKKLQDV 31
|::|| : |||| | : ||: ::
DQ 15 IEVMHYIFGHLNS-EKSTVSSKKKVTRI 40

RESULT 3

A23809
160K antigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jun-2000
C;Accession: A23809; A05268
R;Langley, G.; Scherf, A.; Mercereau-Puijalon, O.; Koenen, M.; Kahane, B.; Mattei, D.; Nucleic Acids Res. 13, 4191-4202, 1985
A;Title: Characterisation of Plasmodium falciparum antigenic determinants isolated from
A;Reference number: A93570; MUID:85242097; PMID:2409532
A;Accession: A23809
A;Molecule type: DNA
A;Residues: 1-70 <LAN>
A;Experimental source: clone ppp2L
C;Comment: This antigen is expressed in all blood stages.
C;Keywords: surface antigen

Query Match 21.8%; Score 39; DB 2; Length 70;
Best Local Similarity 39.1%; Pred. No. 3.6e+02;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 5 IQLMHNIGKHLNSMERVEWLKQDVHNF 27

Db 10 IYILNNIKNLKENVDLNKR 32

RESULT 4

A81898
hypothetical protein NMA1295 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81898
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jägle, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <PAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:G7379742; PIDN:CAB84547.1; PID:G737997
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1295

Query Match 21.5%; Score 38.5; DB 2; Length 61;
Best Local Similarity 30.0%; Pred. No. 3.6e+02;
Matches 9; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 6 QLMNIGKHLNSMERVEWLKQDVHNF 34

Db 22 RLKTVSPHLERKELVDVFMQKEIPDFSNW 51

RESULT 5

S43483
hypothetical protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 01-Feb-1999
C;Accession: S43483
R;Knopp, V.; Brennick, A.
Nucleic Acids Res. 22, 1167-1171, 1994
A;Title: Evidence for a group II intron in Escherichia coli inserted into a highly conse
A;Reference number: S43481; MUID:94218238; PMID:8165129
A;Accession: S43483
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-55 <KNO>

Query Match 21.2%; Score 38; DB 2; Length 55;
Best Local Similarity 30.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 15 LNSMERVEWLKQDVHNF 34
Db 22 LNNVEPKWLVYVIEHQDW 41

RESULT 6

D44088
homotic protein HAT24 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 27-Jun-1994
C;Accession: D44088
R;Schna, M.; Davis, R.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 3894-3898, 1992
A;Title: HD-Zip proteins: members of an Arabidopsis homeodomain protein superfamily.
A;Reference number: A44088; MUID:92237275; PMID:1349174
A;Accession: D44088
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-60 <SCH>
A;Cross-references: GB:M90418

Query Match 21.2%; Score 38; DB 2; Length 60;
Best Local Similarity 29.6%; Pred. No. 4.1e+02;
Matches 8; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 7 LMHNIGKHLNSMERVEWLKQDVHNF 33

Db 5 MNENIEKVLDRGEKTELLVDKTENLRS 31

RESULT 7

T47055
hypothetical protein [imported] - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: T47055
R;Buchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carnie
submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A;Reference number: Z24348
A;Accession: T47055
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-61 <BUC>
A;Cross-references: EMBL:AL031866; PIDN:CAA21398.1
A;Experimental source: strain 6/69

Query Match 21.2%; Score 38; DB 2; Length 61;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 22 EWLKQDVHNF 30

Db 52 EWINKLSD 60

RESULT 8

F85909
hypothetical protein Z3923 [imported] - Escherichia coli (strain O157:H7, substrain EDI
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: F85909
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F85909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <STO>
A;Cross-references: GB:AE005174; NID:G12517055; PIDN:AAG57738.1; GSPDB:GN00145; UWGP:Z3

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 9, 2003, 16:41:11 ; Search time 35 Seconds
(without alignments)
129,443 Million cell updates/sec

US-09-843-221a-16
Protein: GenCore-179
Sequence: SVSEIOLNKLHNSMERVLRKLCLODVNP 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Number of hits satisfying chosen parameters: 507025

Minimum DB seq length: 0

Maximum DB seq length: 70

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Geneseq 101002:
1: /SID82/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:
2: /SID82/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:
3: /SID82/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:
4: /SID82/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:
5: /SID82/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:
6: /SID82/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:
7: /SID82/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:
8: /SID82/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:
9: /SID82/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:
10: /SID82/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:
11: /SID82/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:
12: /SID82/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:
13: /SID82/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:
14: /SID82/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:
15: /SID82/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:
16: /SID82/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:
17: /SID82/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:
18: /SID82/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:
19: /SID82/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:
20: /SID82/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:
21: /SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:
22: /SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:
23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	179	100.0	34	4	Human parathyroid-[Met(O)8,18]hPTH-(Sequence of the fi
2	179	100.0	34	6	Human parathyroid
3	179	100.0	34	7	Parathyroid hormon
4	179	100.0	34	11	[D-Ser3]hPTH (1-34
5	179	100.0	34	13	[Gln25]hPTH (1-34)
6	179	100.0	34	14	[Lys(For)26, Lys(F
7	179	100.0	34	15	[D-Asp30]hPTH(1-3
8	179	100.0	34	15	N-alpha-isopropyl-
9	179	100.0	34	15	
10	179	100.0	34	15	

11	179	100.0	34	15	AA58017	[Lys(N-epsilon-Iso
12	179	100.0	34	15	AA55724	Parathormone N-ter
13	179	100.0	34	16	AA74521	Human parathyroid
14	179	100.0	34	17	AA99449	Human parathyroid
15	179	100.0	34	17	AA99978	Human parathyroid
16	179	100.0	34	17	AA98951	Target peptide (PT
17	179	100.0	34	17	AA98966	PTH(1-34). Not sp
18	179	100.0	34	17	AA88835	Human parathyroid
19	179	100.0	34	18	AA24273	Wild type parathyr
20	179	100.0	34	18	AAW1994	Cyclised human par
21	179	100.0	34	18	AAW2000	Cyclised human par
22	179	100.0	34	18	AAW2006	Cyclised human par
23	179	100.0	34	19	AAW67291	Parathyroid hormon
24	179	100.0	34	19	AAW61658	Parathyroid hormon
25	179	100.0	34	19	AAW65975	Human parathyroid
26	179	100.0	34	20	AAW50593	Resin bound cyclic
27	179	100.0	34	20	AAW17752	Human parathyroid
28	179	100.0	34	20	AAW14151	Human parathyroid
29	179	100.0	34	20	AAW02579	N-terminal 34 resi
30	179	100.0	34	20	AAW81871	Human PTH N-termin
31	179	100.0	34	21	AA307454	Amino acids 1-34 o
32	179	100.0	34	21	AA98017	Human amino-termin
33	179	100.0	34	21	AA982631	Human parathyroid
34	179	100.0	34	21	AAW68763	Amino acids 1-34 o
35	179	100.0	34	22	AA884778	Native rat parathy
36	179	100.0	34	22	AA96898	Human parathyroid
37	179	100.0	34	22	AA881079	Human parathyroid
38	179	100.0	34	22	AA891098	Parathyroid hormon
39	179	100.0	34	23	AAE23727	Human parathyroid
40	179	100.0	34	23	ABB06329	Human parathyroid
41	179	100.0	34	23	ABB08595	C-terminal truncat
42	179	100.0	34	23	AAE18395	Human PTH peptide
43	179	100.0	34	23	ABB07147	Parathyroid hormon
44	179	100.0	34	23	AAU73028	Parathyroid hormon
45	179	100.0	35	22	AA891112	Parathyroid hormon

ALIGNMENTS

RESULT 1
AAP30022
ID AAP30022 standard; peptide; 34 AA.

AC AAP30022;
DT 01-SEP-1992 (first entry)

XX Human parathyroid-(1-34) amide.

XX PTH; parathyroid gland; antibodies.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 34

FT /note= "amidated"

XX JP58096052-A.

XX 07-JUN-1983.

XX 30-NOV-1983; 83JP-0193212.

XX 30-NOV-1981; 81JP-0193212.

XX (TOXN) TOYO JOZO KK.

XX WPI; 1983-709291/28.

XX High activity human parathyroid hormone amide prodn. - by

XX condensing protected aminoacid(s) and/or peptide(s) useful for

XX lowering parathyroid gland function

XX Claim 1; Page 1; 20pp; Japanese.
 XX The human parathyroid hormone, hPTH(1-34)-amide was prep'd. by
 CC the following steps: Firstly the carboxy gp. at the C-terminal
 CC phenylalanine was converted into its amide form. The protected
 CC individual amino acids were condensed, in order, by liquid phase
 CC synthesis. The protecting groups were removed from the N-terminal
 CC amino gp. and other functional gps. by acidolysis, and the
 CC resulting hPTH(1-34)-amide purified by gel filtration
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
 CC column chromatography with carboxymethyl cellulose or ion exchange
 CC resin. The peptide amide is useful in lowering the activity of the
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of
 CC parathyroid gland function.
 XX SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 4; Length 34;
 st Local Similarity 100.0%; Pred. No. 5.7e-16;
 atches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNF 34
 DB 1 SVSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNF 34
 RESULT 2
 AAP50377
 ID AAP50377 standard; peptide; 34 AA.
 XX
 AC AAP50377;
 XX
 DT 08-MAR-1992 (first entry)
 XX
 DE [Met(O)8,18]hPTH-(1-34).
 XX
 DE Human parathyroid hormone; calcium regulation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8 /label= oxidised methionine
 FT Modified-site 18 /label= oxidised methionine
 FT
 XX JP59204159-A.
 PD 19-NOV-1984.
 XX
 PF 28-APR-1983; 83JP-0075607.
 XX
 PR 28-APR-1983; 83JP-0075607.
 XX
 PA (DAIL) DAICEL CHEM IND KK.
 XX
 DR WPI; 1985-003559/01.
 XX
 XX New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in
 PT blood and decreases level in urine.
 PT
 XX Claim 1; Page 1; 3pp; Japanese.
 XX Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,
 CC decreases Ca in urine and increases P in urine by increasing cAMP in
 CC urine and enhancing vitamin D hydroxylase activity in kidneys. The
 CC modified derivative only has the effect of lowering Ca levels in
 CC urine and can be used when only this particular effect is required.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 6; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNF 34
 DB 1 SVSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNF 34
 RESULT 3
 AAP60031
 ID AAP60031 standard; peptide; 34 AA.
 XX
 AC AAP60031;
 XX
 DT 06-JUL-1991 (first entry)
 XX
 DE Sequence of the first 34 AA residues of a parathyroid hormone
 DE obtainable from a human or animal.
 XX
 KW Osteoporosis therapy.
 XX
 OS Homo sapiens/animal.
 XX
 XX EP197514-A.
 FN
 XX
 PD 15-OCT-1986.
 XX
 PF 03-APR-1986; 86EP-0104562.
 XX
 PR 04-APR-1985; 85US-0720018.
 PR 05-DEC-1986; 86US-0939308.
 PR 21-MAY-1987; 87US-0052383.
 XX
 FA (GEHO-) GEN HOSPITAL CORP.
 XX
 PI Potts JT, Neer RM, Slovick DM;
 XX
 XX WPI; 1986-273437/42.
 DR
 XX Compn. and kits for increasing bone mass in osteoporosis -
 PT contg. parathyroid hormone or fragment with hydroxylated
 PT vitamin/D cpd. or calcium salt
 XX
 PS Claim 4; Page 24; 26pp; English.
 XX
 CC The peptide is used in a pharmaceutical compsn. together with a
 CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.
 CC CaCO3. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-
 CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-
 CC hydroxy vitamin D2 or 1-alpha,25-dihydroxy vitamin D2.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 7; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNF 34
 DB 1 SVSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNF 34
 RESULT 4
 AAR07919
 ID AAR07919 standard; protein; 34 AA.
 XX
 AC AAR07919;
 XX
 DT 18-FEB-1991 (first entry)
 XX
 DE Human parathyroid hormone analogue, hPTH(7-34).
 XX
 KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.

XX OS Homo sapiens.
 XX PD US4968669-A.
 XX PF 06-NOV-1990.
 XX PP 21-APR-1989; 89US-0341597.
 XX PR 21-APR-1989; 89US-0341597.
 XX PR 09-MAY-1988; 88US-0191512.
 XX PA (MERI) MERCK & CO INC.
 XX PI Rosenblatt M, Chorev M;
 XX WPI; 1990-354642/47.
 XX SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5,7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT New para:thyroid hormone analogues - which inhibit hormone
 PT activity by binding receptors while not producing second
 PT messenger molecules
 PS Claim 1; Column 8; 6pp; English.
 XX Peptide analogues have high affinity for PTH cell surface receptors,
 CC but do not stimulate production of secondary messenger molecules.
 CC They may be used in inhibition of PTH action, and in diagnosis and
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
 CC Analogues may also be used in treatment of tumours and other cells
 CC overproducing peptide hormone-like substances, and immune diseases
 CC eg. allergic inflammation and hyperactive lymphocytes.
 CC Naturally occurring PTH levels may also be measured in vitro.
 XX SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5,7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
 DB 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
 RESULT 5
 AAR22283
 ID AAR22283 standard; peptide; 34 AA.
 XX AAR22283;
 DT 29-JUL-1992 (first entry)
 XX Parathyroid hormone analogue N-terminus [1-34].
 XX Human; hPTH; wound healing; hair growth; hyperproliferation skin;
 KW disorders; psoriasis; cancer; burns.
 XX Homo sapiens.
 XX WO9204039-A.
 XX PD 19-MAR-1992.
 XX PF 30-AUG-1991; 91WO-US06218.
 XX PR 30-AUG-1990; 90US-0575219.
 XX PA (HOLI/) HOLICK M F.
 XX PI Hollick MF;
 XX WPI; 1992-114063/14.

PT Use of peptide having homology with parathyroid hormone - for
 PT enhancement of cell proliferation for wound healing
 XX Disclosure; Fig 1; 34pp; English.
 XX The peptide can be easily synthesised by recombinant DNA or solid
 CC phase peptide synthesis techniques. The peptide has > 50 percent
 CC homology with the N-terminal 1-34 amino acids of human parathyroid
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The
 CC peptide may be used in a method for the treatment of hyperprolifer-
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin
 CC ulcerations by inhibition of cell proliferation and enhancement of
 CC cell differentiation (agonist activity). They are also used to
 CC enhance cell proliferation (antagonist activity) for wound healing.
 CC They are also applicable in the promotion of new hair growth or
 CC stimulation of the rate of hair growth e.g. following chemotherapy
 CC or for treating alopecia e.g. male pattern baldness.
 XX SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5,7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
 DB 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
 RESULT 6
 AAR41549
 ID AAR41549 standard; protein; 34 AA.
 XX AAR41549;
 XX DT 11-APR-1994 (first entry)
 XX DE [D-Ser3]hPTH (1-34)NH2.
 XX KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 3 /note = "D-form residue"
 FT Modified-site 34 /note = "C terminal is amidated"
 XX EP561412-A.
 XX PD 22-SEP-1993.
 XX PF 18-MAR-1993; 93EP-0104500.
 XX PR 19-MAR-1992; 92JP-0063517.
 XX PR 18-FEB-1993; 93JP-0029283.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Fukuda T, Nakagawa S, Taketomi S;
 XX WPI; 1993-296712/38.
 XX PT New parathyroid hormone deriva. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX Example 1; Page 17; 37pp; English.
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is

CC obtained. The proteins can be used to treat a number of bone and blood disorders. This analogue was used as a test compound.

XX Sequence 34 AA;
Query Match 100.0%; Score 179; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 5,7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
Db 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34

RESULT 7

AAR41570
ID AAR41570 standard; protein; 34 AA.

XX AAR41570;

b. 11-APR-1994 (first entry)

XX [Gln25]hPTH (1-34).

XX PTH; parathyroid hormone; protease resistance; osteoporosis;
KW hypoparathyroidism; hypertension.

XX Homo sapiens.

XX EP561412-A.

XX 22-SEP-1993.

XX 18-MAR-1993; 93EP-0104500.

XX 19-MAR-1992; 92JP-0063517.

XX 18-FEB-1993; 93JP-0029283.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Fukuda T, Nakagawa S, Taketomi S;

DR WPI; 1993-296712/38.

XX New parathyroid hormone derivs. - used for the treatment of

PT osteoporosis hypoparathyroidism and hypertension

XX Example 1; Page 27; 37pp; English.

CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
CC AAR41549-R41582 - specific examples) show increased resistance to
CC proteases and a greater persistency of activity within the blood is
CC obtained. The proteins can be used to treat a number of bone and blood
CC disorders. This analogue was used as a test compound.

XX Sequence 34 AA;
Query Match 100.0%; Score 179; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 5,7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34
Db 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

AAR58291
ID AAR58291 standard; peptide; 34 AA.

XX AAR58291;

XX 20-SEP-1994 (first entry)

XX [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.
DE Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
OS Synthetic.

XX Key Location/Qualifiers
FH Modified-site 26 /label= Other
FT /note= "Formyl-Lys."
FT Modified-site 27 /label= Other
FT /note= "Formyl-Lys."
FT Modified-site 34 /note= "in amide form"

XX GB2269176-A.

XX 02-FEB-1994.

XX 12-JUL-1993; 93GB-0014384.

XX 15-JUL-1992; 92GB-0015009.

XX 18-DEC-1992; 92GB-0026415.

XX 23-DEC-1992; 92GB-0026859.

XX 23-DEC-1992; 92GB-0026861.

XX 28-JAN-1993; 93GB-0001691.

XX 28-JAN-1993; 93GB-0001692.

XX 14-APR-1993; 93GB-0007673.

XX 19-APR-1993; 93GB-0008033.

XX (SANO) SANDOZ LTD.

PA (BAUTE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX WPI; 1994-018352/03.

XX New active para-thyroid hormone variants - used for treating or

PT preventing osteoporosis etc.

XX Example 289; Page 47; 92pp; English.

XX This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX Sequence 34 AA;

Query Match 100.0%; Score 179; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 5,7e-16;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34

Db 1 SVSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9

AAR58228

ID AAR58228 standard; peptide; 34 AA.

XX

XX AAR58228;

DT 20-SEP-1994 (first entry)
 XX [D-Asp30]-hPTH(1-34)-NH2.
 DE Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteoporosis;
 KW hypoparathyroidism.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 30 /note= "D-form residue."
 FT Modified-site 34 /note= "in amide form"
 FT
 FT
 FT
 XX GB2269176-A.
 PN
 XX
 PD 02-FEB-1994.
 XX
 XX 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 226; Page 45; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMNLGKHLNSMERVWLKKLQDVHNF 34
 DB 1 SVSEIQLMNLGKHLNSMERVWLKKLQDVHNF 34
 RESULT 10
 AAR58016
 ID AAR58016 standard; peptide; 34 AA.
 XX
 AC AAR58016;
 XX
 XX 20-SEP-1994 (first entry)
 DE N-alpha-Isopropyl-hPTH(1-34)-NH2 parathyroid hormone variant.

XX Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteoporosis;
 KW hypoparathyroidism.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-alpha-isopropyl-Ser"
 FT Modified-site 34 /note= "in amide form"
 FT
 FT
 FT
 XX GB2269176-A.
 PN
 XX
 PD 02-FEB-1994.
 XX
 XX 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 1; Page 30; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 179; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMNLGKHLNSMERVWLKKLQDVHNF 34
 DB 1 SVSEIQLMNLGKHLNSMERVWLKKLQDVHNF 34
 RESULT 11
 AAR58017
 ID AAR58017 standard; peptide; 34 AA.
 XX
 AC AAR58017;
 XX
 XX 20-SEP-1994 (first entry)
 DE [Lys(N-epsilon-Isopropyl)26,27]-human parathyroid hormone(1-34)-NH2.
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteoporosis;
 KW hypoparathyroidism.

XX hypoparathyroidism.
OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 26 /note= "N-epsilon-Isopropyl-Lys"
FT Modified-site 27 /note= "N-epsilon-Isopropyl-Lys"
FT Modified-site 34 /note= "in amide form"
FT
XX GB2269176-A.
PN
XX
PD 02-FEB-1994.
XX
XX 12-JUL-1993; 93GB-0014384.
XX
XX 15-JUL-1992; 92GB-0015009.
XX 18-DEC-1992; 92GB-0026415.
XX 23-DEC-1992; 92GB-0026859.
XX 23-DEC-1992; 92GB-0026861.
XX 28-JAN-1993; 93GB-0001691.
XX 28-JAN-1993; 93GB-0001692.
XX 14-APR-1993; 93GB-0007673.
XX 19-APR-1993; 93GB-0008033.
XX (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX Albert R, Bauer W, Breckenridge R, Cardinaux P;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
XX WPI; 1994-018352/03.
XX
XX New active para-thyroid hormone variants - used for treating or
FT preventing osteoporosis etc.
PT
XX
XX Example 2; Page 32; 92pp; English.
XX
XX This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
SQ Sequence 34 AA;
Query Match 100.0%; Score 179; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 5,7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34
RESULT 12
AAR55724
ID AAR55724 standard; peptide; 34 AA.
XX
AC AAR55724;
XX
DT 16-NOV-1994 (first entry)
XX
XX Parathormone N-terminal sequence.
XX
XX Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;
KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; EPA;
KW eicosapentaenoic acid; EPA; antitumor.

XX Synthetic.
OS WO9412530-A.
XX
XX 09-JUN-1994.
PD
XX
XX 29-NOV-1993; 93WO-HU00065.
XX
XX 30-NOV-1992; 92US-0984293.
XX
XX (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
PA (SYNT-) SYNTHETIC PEPTIDES INC.
PA
XX Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;
PI Szederkenyi F, Vadasz Z;
PI
XX WPI; 1994-200194/24.
XX
XX New fatty acyl-peptide conjugates for inhibiting cell
PT proliferation - more active than free peptide, partic. for
PT treating tumours, virus-infected cells, psoriasis, etc.
XX
XX Disclosure; Fig. 1; 45pp; English.
XX
XX The peptides given in AAR55718-48 can each be conjugated through an
CC amide linkage with a polyunsaturated fatty acid moiety, such as
CC docosahexaenoic acid (DHA) or eicosapentaenoic acid, to improve
CC antiproliferative activity. The parathormone N-terminal fragment
CC inhibits osteoblast proliferation.
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 179; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 5,7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34
RESULT 13
AAR74521
ID AAR74521 standard; Peptide; 34 AA.
XX
AC AAR74521;
XX
XX 04-DEC-1995 (first entry)
DT
XX Human parathyroid hormone (1-34).
DE
XX Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
XX osteoporosis; hypercalcaemia; hyperparathyroidism;
KW metabolic bone disease; human; veterinary medicine;
KW iontophoretic transdermal transport; recombinant E.coli.
XX
XX Homo sapiens.
OS
XX WO9511988-A.
PN
XX 04-MAY-1995.
PD
XX 25-OCT-1994; 94WO-US12205.
XX
XX 25-OCT-1993; 93US-0142551.
XX
XX (APFY-) APFYMEX TECHNOLOGIES NV.
PA
XX Oldenburg KR, Selick HE;
PI
XX WPI; 1995-178880/23.
DR
XX

PT New active analogues of parathyroid hormone - with increased
PT activity, stability in serum etc., esp. for treating
XX osteoporosis, also related DNA and vectors
PS Disclosure; Page 1; 109pp; English.
XX
CC This sequence represents residues 1-34 of human parathyroid hormone
CC (RPTH). This sequence was used in the production of analogues of the
CC truncated form of PTH. These analogues have increased activity and
CC longer serum half life than native PTH due to eg. substitution of Met
CC residues with Leu residues and replacing the carboxy Phe with Tyr. The
CC carboxy terminal may also be modified by the addition of a homoserine
CC residue or analogue, or by the addition of residues 35-84 of wild type
CC PTH (see AAR74410). These PTH analogues may be used in the treatment of
CC osteoporosis or hypercalcaemia, hyperparathyroidism or other metabolic
CC bone diseases in human or veterinary medicine. These peptides may also
CC have increased iontophoretic transdermal transport compared to wild type
CC PTH and can be produced in high yield in recombinant E.coli.
XX
SQ Sequence 34 AA;

XX Query Match 100.0%; Score 179; DB 16; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 5.7e-16;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 SVSEIQLMNLGKHLNSMERVEWLKKLQDVHNF 34
XX |||||
XX 1 SVSEIQLMNLGKHLNSMERVEWLKKLQDVHNF 34
XX |||||

XX RESULT 14
XX AAW99449
XX ID AAW99449 standard; peptide; 34 AA.
XX
XX AC AAW99449;
XX
XX DT 08-JUN-1999 (first entry)
XX
XX DE Human parathyroid hormone aal-34.
XX
XX KW Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;
XX spontaneous abortion; uterine contraction; human.
XX
XX OS Homo sapiens.
XX
XX PN US5880093-A.
XX
XX PD 09-MAR-1999.
XX
XX PR 05-APR-1995; 95US-0411726.
XX
XX PA 28-SEP-1992; 92IT-MI02331.
XX
XX PI (BAGN/) BAGNOLI F.
XX
XX PI Bagnoli F;
XX
XX DR WPI; 1996-162392/17.
XX
XX PT Use of composition containing parathormone or fragments - for
XX preventing premature birth or spontaneous abortion or for treating
XX unwanted uterine contractions
XX
XX PS Disclosure; Column 7-8; 11pp; English.
XX
XX CC Peptides AAW99448-W99452 represent all or part of the parathyroid
XX hormone (PTH; parathormone) sequence or related peptide. The peptides
XX are used for preventing premature birth, spontaneous abortion or unwanted
XX uterine contractions in a pregnant human patient.
XX (Note: this patent is the first Major Country Equivalent to Italian
XX Patent IT1255388).
XX
XX SQ Sequence 34 AA;

Query Match 100.0%; Score 179; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 SVSEIQLMNLGKHLNSMERVEWLKKLQDVHNF 34
XX |||||
XX 1 SVSEIQLMNLGKHLNSMERVEWLKKLQDVHNF 34
XX |||||

XX RESULT 15
XX AAR99978
XX ID AAR99978 standard; peptide; 34 AA.
XX
XX AC AAR99978;
XX
XX DT 30-APR-1997 (first entry)
XX
XX DE Human parathyroid hormone peptide fragment (1-34).
XX
XX KW cyclic parathyroid hormone fragment; calcium-regulating activity;
XX osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
XX improved half life; calcium retention; bone.
XX
XX OS Synthetic.
XX
XX PN DE19508672-A1.
XX
XX PD 12-SEP-1996.
XX
XX PR 10-MAR-1995; 95DE-1008672.
XX
XX PR 10-MAR-1995; 95DE-1008672.
XX
XX PA (BOEF) BOEHRINGER MANNHEIM GMBH.
XX
XX PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;
XX WPI; 1996-413519/42.
XX
XX DR Cyclic parathyroid hormone fragments with lactam bridge - have good
XX in vivo half life and are useful for treating osteoporosis and
XX preventing epidermal cell proliferation
XX
XX PS Disclosure; Page 9; 14pp; German.
XX
XX CC New cyclic parathyroid hormone fragments (CPTH) have the amino acid
XX sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino
XX acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
XX the N-terminus, and are cyclised between positions 13 and 17. One of
XX these positions is occupied by L- or D- Orn or Lys, and the other by L-
XX or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
XX treating osteoporosis and inhibit proliferation of epidermal cells (for
XX treating psoriasis). The CPTH have an improved half life in vivo than
XX known PTH fragments, increased mitogenicity and DNA-synthesising
XX capacity, reduced catabolic, calcium-mobilising activity and increased
XX activity for calcium retention and incorporation into bone. The
XX present sequence is that of human PTH peptide fragment (1-34).
XX
XX SQ Sequence 34 AA;

XX Query Match 100.0%; Score 179; DB 17; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 5.7e-16;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 SVSEIQLMNLGKHLNSMERVEWLKKLQDVHNF 34
XX |||||
XX 1 SVSEIQLMNLGKHLNSMERVEWLKKLQDVHNF 34
XX |||||

XX Search completed: April 9, 2003, 16:44:14
XX Job time : 37 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4 ps 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 9, 2003, 16:43:37 ; Search time 15 Seconds
(without alignments)
66.692 Million cell updates/sec

Title: US-09-843-221A-16

Sequence: 1 SVSEIQLMHLNKLNSMERVWLKQLQDVHNF 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

number of hits satisfying chosen parameters: 189198

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents-AA:
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	100.0	34	1 US-07-765-373-1	Sequence 1, Appli
2	179	100.0	34	1 US-08-033-099-1	Sequence 1, Appli
3	179	100.0	34	1 US-08-262-495C-1	Sequence 1, Appli
4	179	100.0	34	1 US-07-915-247A-1	Sequence 1, Appli
5	179	100.0	34	1 US-08-443-863-1	Sequence 1, Appli
6	179	100.0	34	1 US-08-448-070-1	Sequence 1, Appli
7	179	100.0	34	1 US-08-488-105-7	Sequence 1, Appli
8	179	100.0	34	1 US-08-468-275-6	Sequence 6, Appli
9	179	100.0	34	1 US-08-449-500-1	Sequence 1, Appli
10	179	100.0	34	1 US-08-449-317A-1	Sequence 1, Appli
11	179	100.0	34	2 US-08-142-551B-2	Sequence 2, Appli
12	179	100.0	34	2 US-08-477-022-1	Sequence 1, Appli
13	179	100.0	34	2 US-08-449-447-1	Sequence 1, Appli
14	179	100.0	34	2 US-08-835-231-13	Sequence 13, Appli
15	179	100.0	34	2 US-08-184-328-1	Sequence 1, Appli
16	179	100.0	34	2 US-08-411-726-2	Sequence 2, Appli
17	179	100.0	34	2 US-08-691-647C-5	Sequence 5, Appli
18	179	100.0	34	2 US-08-521-097-1	Sequence 1, Appli
19	179	100.0	34	3 US-09-044-536A-1	Sequence 1, Appli
20	179	100.0	34	3 US-08-904-760B-22	Sequence 22, Appli
21	179	100.0	34	4 US-09-108-661-13	Sequence 13, Appli
22	179	100.0	34	4 US-09-007-466-6	Sequence 6, Appli
23	179	100.0	34	4 US-09-406-813-1	Sequence 1, Appli
24	179	100.0	34	4 US-08-952-980B-6	Sequence 6, Appli
25	179	100.0	34	5 PCT-US95-15800-22	Sequence 22, Appli
26	179	100.0	35	1 US-08-256-363-3	Sequence 3, Appli
27	179	100.0	36	1 US-08-256-363-4	Sequence 4, Appli

28	179	100.0	37	1 US-08-440-117-1	Sequence 1, Appli
29	179	100.0	37	4 US-09-068-738A-16	Sequence 16, Appli
30	179	100.0	38	1 US-08-112-024-1	Sequence 1, Appli
31	179	100.0	38	1 US-08-232-849-1	Sequence 1, Appli
32	179	100.0	38	2 US-08-625-586-1	Sequence 1, Appli
33	179	100.0	38	3 US-09-128-401-1	Sequence 1, Appli
34	176	98.3	34	4 US-08-903-497A-1	Sequence 1, Appli
35	176	98.3	34	4 US-09-635-076-1	Sequence 1, Appli
36	175	97.8	34	1 US-08-488-105-1	Sequence 1, Appli
37	175	97.8	34	1 US-08-488-105-13	Sequence 13, Appli
38	175	97.8	36	1 US-08-112-024-2	Sequence 2, Appli
39	174	97.2	34	3 US-09-044-536A-9	Sequence 9, Appli
40	173	96.6	34	3 US-09-044-536A-10	Sequence 10, Appli
41	173	96.6	34	3 US-08-904-760B-9	Sequence 9, Appli
42	172	96.1	34	1 US-08-262-495C-2	Sequence 2, Appli
43	172	96.1	34	3 US-09-044-536A-13	Sequence 13, Appli
44	172	96.1	34	3 US-09-044-536A-14	Sequence 14, Appli
45	172	96.1	34	3 US-09-044-536A-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-07-765-373-1
Sequence 1, Application US/07765373
Patent No. 5393869
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, Shizue
APPLICANT: FUKUDA, Teunehiko
APPLICANT: KAWASE, Masahiro
APPLICANT: YAMAZAKI, Iwao
TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/765,373
FILING DATE: 19910925
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: 41289
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 20991 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-07-765-373-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHLNKLNSMERVWLKQLQDVHNF 34

Db 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

RESULT 2

US-08-033-099-1

; Sequence 1, Application US/08033099

; Patent No. 5434246

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

; ADDRESSEE: CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/033,099

; FILING DATE: 19930316

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAMS, Gregory D

; REGISTRATION NUMBER: 30901

; REFERENCE/DOCKET NUMBER: 42528

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (613)523-6440

; TELEX: 200291 STRE UR

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: N-terminal

US-08-033-099-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qv 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

Db 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

RESULT 3

US-08-262-495C-1

; Sequence 1, Application US/08262495C

; Patent No. 5556940

; GENERAL INFORMATION:

; APPLICANT: WILLICK, Gordon E.

; APPLICANT: WHITFIELD, James F.

; APPLICANT: SUREWICZ, Witold

; APPLICANT: SUNG, Wing L.

; APPLICANT: NEUGENBAUER, Witold

; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kirby, Eades, Gale, Baker

; STREET: 112 Kent Street, Suite 770,

City: Ottawa
Country: Canada
Computer Readable Form:
Medium Type: Floppy disk
Computer: IBM PC Compatible
Operating System: PC-DOS/MS-DOS
Software: Wordperfect 5.1
Current Application Data:
Application Number: US/08/262,495C
Filing Date:
Classification: 530
Prior Application Data:
Application Number:
Filing Date:
Classification: 530
Attorney/Agent Information:
Name: EADES, No. 5556940ris M.
Registration Number: 5,263
Reference/Docket Number: 36210
Telecommunication Information:
Telephone: (613)-237-6900
Telefax: (613)-237-0045

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-262-495C-1

Query Match 100.0%; Score 179; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.8e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qv 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

Db 1 SVSEIQLMHNLGKHLNSMVERVWLKRLQDVHNF 34

RESULT 4

US-07-915-247A-1

; Sequence 1, Application US/07915247A

; Patent No. 5589452

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/915,247A

; FILING DATE: 19920714

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-07-915-247A-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNGLKHLNSMERVWLKQLQDVHNF 34
|||
DB 1 SVSEIQLMHNGLKHLNSMERVWLKQLQDVHNF 34

RESULT 5
US-08-443-863-1
Sequence 1, Application US/08443863
Patent No. 5693616
GENERAL INFORMATION:

APPLICANT: Kristenansky, John L.
APPLICANT: Nestor Jr., John J.
APPLICANT: Ho, Teresa H.
APPLICANT: Vickery, Brian H.
APPLICANT: Bach, Chinh T.
TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,863
FILING DATE: 14-JUL-1992
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-443-863-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNGLKHLNSMERVWLKQLQDVHNF 34
|||
DB 1 SVSEIQLMHNGLKHLNSMERVWLKQLQDVHNF 34

RESULT 6

US-08-448-070-1
Sequence 1, Application US/08448070
Patent No. 5695955
GENERAL INFORMATION:

APPLICANT: Kristenansky, John L.
APPLICANT: Nestor Jr., John J.
APPLICANT: Ho, Teresa H.
APPLICANT: Vickery, Brian H.
APPLICANT: Bach, Chinh T.
TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,070
FILING DATE: 14-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-448-070-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNGLKHLNSMERVWLKQLQDVHNF 34
|||
DB 1 SVSEIQLMHNGLKHLNSMERVWLKQLQDVHNF 34

RESULT 7

US-08-488-105-7
Sequence 7, Application US/08488105
Patent No. 5717062
GENERAL INFORMATION:

APPLICANT: Choev, Michael
APPLICANT: Rosenblatt, Michael
TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,105
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
REGISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 00537/112001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: The side chains of Lys at position 26 and Asp at position 30 are linked by an amide bond and this sequence has an amide C-terminus (i.e., CONH2), rather than a carboxy C-terminus (i.e., COOH).
US-08-488-105-7

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3,8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNGLGKHLNSMERVWLKRLQDVHNF 34
|||||
Db 1 SVSEIQLMHNGLGKHLNSMERVWLKRLQDVHNF 34

RESULT 8
US-08-468-275-6
Sequence 6, Application US/08468275
Patent No. 5747453
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661

REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-275-6

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3,8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNGLGKHLNSMERVWLKRLQDVHNF 34
|||||
Db 1 SVSEIQLMHNGLGKHLNSMERVWLKRLQDVHNF 34

RESULT 9
US-08-449-500-1
Sequence 1, Application US/08449500
Patent No. 5798225
GENERAL INFORMATION:
APPLICANT: Kristiansky, John L.
APPLICANT: Nestor Jr., John J.
APPLICANT: Ho, Teresa H.
APPLICANT: Vickery, Brian H.
APPLICANT: Bach, Chinh T.
TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
FOR THE TREATMENT OF OSTEOPOROSIS
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,500
FILING DATE: 18-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-449-500-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3,8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34
Db 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 10

US-08-449-317A-1
; Sequence 1, Application US/08449317A
; Patent No. 5807823
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,317A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610-P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-449-317A-1

Query Match 100.0%; Score 179; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34
Db 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 11

US-08-142-551B-2
; Sequence 2, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..34
OTHER INFORMATION: /note= "The sequence of the 34
OTHER INFORMATION: amino acid truncated human PTH peptide,
OTHER INFORMATION: designated: Human PTH."
US-08-142-551B-2

Query Match 100.0%; Score 179; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34
Db 1 SVSEIQLMNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 12

US-08-477-022-1
; Sequence 1, Application US/08477022
; Patent No. 5821225
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,022
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 27610-P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6593
TELEFAX: 415-496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-477-022-1

Query Match	Score	DB 2	Length
Best Local Similarity	100.0%	179	34
atthes 34	100.0%	Pred. No. 3	8e-17
Conservative	0	Mismatches	0
Indels	0	Gaps	0

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13
US-08-449-447-1
; Sequence 1, Application US/08449447
; Patent No. 5840837
; GENERAL INFORMATION:
; APPLICANT: Krestenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,447
FILING DATE: 18-JAN-1994

```
Query Match      100.0%; Score 179; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels
```

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
 |||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14
US-08-835-231-13
; Sequence 13, Application US/08835231
; Patent No. 5861284
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 5861284nyuki
; APPLICANT: FUKUDA, Taunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 179; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 34; Conservative 0; Mismatches 0; Indels

QY 1 SVSEIQLMHNGLGKHLNSMERVEWLKKLQDVHNF 34

Db 1 SVSEIQLMHNLGKHLNSMERVWLRRKKLQDVHNF 34

RESULT 15

US-08-184-328-1

; Sequence 1, Application US/08184328

; Patent No. 5874086

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/184,328

; FILING DATE: 18-JAN-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

; US-08-184-328-1

Query Match 100.0%; Score 179; DB 2; Length 34;

Best Local Similarity 100.0%; Fred. No. 3.8e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVWLRRKKLQDVHNF 34

Db 1 SVSEIQLMHNLGKHLNSMERVWLRRKKLQDVHNF 34

Search completed: April 9, 2003, 16:45:51

Job time : 16 secs

T...

SPTO)

THIS PAGE BLANK (USPTO)